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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/674,035A

DATE: 07/12/2002

TIME: 10:40:08

Input Set : A:\227274078.ST25.txt

Output Set: N:\CRF3\07122002\I674035A.raw

3 <110> APPLICANT: Lang, Jas C.
 5 <120> TITLE OF INVENTION: Detecting the Expression of the DESC1 Gene in Squamous Cell
 Carcinoma

7 <130> FILE REFERENCE: 22727/04078
 9 <140> CURRENT APPLICATION NUMBER: 09/674,035A
 10 <141> CURRENT FILING DATE: 2000-12-11
 12 <150> PRIOR APPLICATION NUMBER: PCT/IB99/01818
 13 <151> PRIOR FILING DATE: 1999-11-11
 15 <160> NUMBER OF SEQ ID NOS: 10
 17 <170> SOFTWARE: PatentIn version 3.1
 19 <210> SEQ ID NO: 1
 20 <211> LENGTH: 1269
 21 <212> TYPE: DNA
 22 <213> ORGANISM: DESC1
 24 <220> FEATURE:
 25 <221> NAME/KEY: CDS
 26 <222> LOCATION: (1)..(1269)
 27 <223> OTHER INFORMATION:

30 <400> SEQUENCE: 1

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32	Met Tyr Arg Pro Asp Val Val Arg Ala Arg Lys Arg Val Cys Trp Glu	
33	1 5 10 15	
35	ccc tgg gtt atc ggc ctc gtc atc ttc ata tcc ctg att gtc ctg gca	96
36	Pro Trp Val Ile Gly Leu Val Ile Phe Ile Ser Leu Ile Val Leu Ala	
37	20 25 30	
39	gtg tgc att gga ctc act gtt cat tat gtg aga tat aat caa aag aag	144
40	Val Cys Ile Gly Leu Thr Val His Tyr Val Arg Tyr Asn Gln Lys Lys	
41	35 40 45	
43	acc tac aat tac tat agc aca ttg tca ttt aca act gac aaa cta tat	192
44	Thr Tyr Asn Tyr Tyr Ser Thr Leu Ser Phe Thr Thr Asp Lys Leu Tyr	
45	50 55 60	
47	gct gag ttt ggc aga gag gct tct aac aat ttt aca gaa atg agc cag	240
48	Ala Glu Phe Gly Arg Glu Ala Ser Asn Asn Phe Thr Glu Met Ser Gln	
49	65 70 75 80	
51	aga ctt gaa tca atg gtg aaa aat gca ttt tat aaa tct cca tta agg	288
52	Arg Leu Glu Ser Met Val Lys Asn Ala Phe Tyr Lys Ser Pro Leu Arg	
53	85 90 95	
55	gaa gaa ttt gtc aag tct cag gtt atc aag ttc agt caa cag aag cat	336
56	Glu Glu Phe Val Lys Ser Gln Val Ile Lys Phe Ser Gln Gln Lys His	
57	100 105 110	
59	gga gtg ttg gct cat atg ctg ttg att tgt aga ttt cac tct act gag	384
60	Gly Val Leu Ala His Met Leu Leu Ile Cys Arg Phe His Ser Thr Glu	
61	115 120 125	
63	gat cct gaa act gta gat aaa att gtt caa ctt gtt tta cat gaa aag	432

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64	Asp	Pro	Glu	Thr	Val	Asp	Lys	Ile	Val	Gln	Leu	Val	Leu	His	Glu	Lys	
65	130				135				140								
67	ctg	caa	gat	gct	gta	gga	ccc	cct	aaa	gta	gat	cct	cac	tca	gtt	aaa	480
68	Leu	Gln	Asp	Ala	Val	Gly	Pro	Pro	Lys	Val	Asp	Pro	His	Ser	Val	Lys	
69	145				150				155				160				
71	att	aaa	aaa	atc	aac	aag	aca	gaa	aca	gac	agc	tat	cta	aac	cat	tgc	528
72	Ile	Lys	Lys	Ile	Asn	Lys	Thr	Glu	Thr	Asp	Ser	Tyr	Leu	Asn	His	Cys	
73					165			170				175					
75	tgc	gga	aca	cga	aga	agt	aaa	act	cta	ggt	cag	agt	ctc	agg	atc	gtt	576
76	Cys	Gly	Thr	Arg	Arg	Ser	Lys	Thr	Leu	Gly	Gln	Ser	Leu	Arg	Ile	Val	
77					180			185			190						
79	ggt	ggg	aca	gaa	gta	gaa	gag	ggt	gaa	tgg	ccc	tgg	cag	gct	agc	ctg	624
80	Gly	Gly	Thr	Glu	Val	Glu	Gly	Glu	Gly	Trp	Pro	Trp	Gln	Ala	Ser	Leu	
81					195			200			205						
83	cag	tgg	gat	ggg	agt	cat	gcg	tgt	gga	gca	acc	tta	att	aat	gcc	aca	672
84	Gln	Trp	Asp	Gly	Ser	His	Ala	Cys	Gly	Ala	Thr	Leu	Ile	Asn	Ala	Thr	
85					210			215			220						
87	tgg	ctt	gtg	agt	gct	cac	tgt	ttt	aca	aca	tat	aag	aac	cct	gcc		720
88	Trp	Leu	Val	Ser	Ala	Ala	His	Cys	Phe	Thr	Thr	Tyr	Lys	Asn	Pro	Ala	
89	225				230			235			240						
91	aga	tgg	act	gct	tcc	ttt	gga	gta	aca	ata	aaa	cct	tgc	aaa	atg	aaa	768
92	Arg	Trp	Thr	Ala	Ser	Phe	Gly	Val	Thr	Ile	Lys	Pro	Ser	Lys	Met	Lys	
93					245			250			255						
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96	Arg	Gly	Leu	Arg	Arg	Ile	Ile	Val	His	Glu	Lys	Tyr	Lys	His	Pro	Ser	
97					260			265			270						
99	cat	gac	tat	gat	att	tct	ctt	gca	gag	ctt	tct	agc	cct	gtt	ccc	tac	864
100	His	Asp	Tyr	Asp	Ile	Ser	Leu	Ala	Glu	Leu	Ser	Ser	Pro	Val	Pro	Tyr	
101					275			280			285						
103	aca	aat	gca	gta	cat	aga	gtt	tgt	ctc	cct	gat	gca	tcc	tat	gag	ttt	912
104	Thr	Asn	Ala	Val	His	Arg	Val	Cys	Leu	Pro	Asp	Ala	Ser	Tyr	Glu	Phe	
105					290			295			300						
107	caa	cca	ggt	gat	gtg	atg	ttt	gtg	aca	gga	ttt	gga	gca	ctg	aaa	aat	960
108	Gln	Pro	Gly	Asp	Val	Met	Phe	Val	Thr	Gly	Phe	Gly	Ala	Leu	Lys	Asn	
109	305				310			315			320						
111	gat	ggt	tac	agt	caa	aat	cat	ctt	cga	caa	gca	cag	gtg	act	ctc	ata	1008
112	Asp	Gly	Tyr	Ser	Gln	Asn	His	Leu	Arg	Gln	Ala	Gln	Val	Thr	Leu	Ile	
113					325			330			335						
115	gac	gct	aca	act	tgc	aat	gaa	cct	caa	gct	tac	aat	gac	gcc	ata	act	1056
116	Asp	Ala	Thr	Thr	Cys	Asn	Glu	Pro	Gln	Ala	Tyr	Asn	Asp	Ala	Ile	Thr	
117					340			345			350						
119	cct	aga	atc	tta	tgt	gct	ggc	tcc	tta	gaa	gga	aaa	aca	gat	gca	tgc	1104
120	Pro	Arg	Ile	Leu	Cys	Ala	Gly	Ser	Leu	Glu	Gly	Lys	Thr	Asp	Ala	Cys	
121					355			360			365						
123	cag	ggt	gac	tct	gga	gga	cca	ctg	gtt	agt	tca	gat	gct	aga	gat	atc	1152
124	Gln	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Val	Ser	Ser	Asp	Ala	Arg	Asp	Ile	
125					370			375			380						
127	tgg	tac	ctt	gct	gga	ata	gtg	agc	tgg	gga	gat	gaa	tgt	gca	aaa	ccc	1200
128	Trp	Tyr	Leu	Ala	Gly	Ile	Val	Ser	Trp	Gly	Asp	Glu	Cys	Ala	Lys	Pro	

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132	Asn Lys Pro Gly Val Tyr Thr Arg Val Thr Ala Leu Arg Asp Trp Ile				
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151	Pro Trp Val Ile Gly Leu Val Ile Phe Ile Ser Leu Ile Val Leu Ala				
152	20 25 30				
155	Val Cys Ile Gly Leu Thr Val His Tyr Val Arg Tyr Asn Gln Lys Lys				
156	35 40 45				
159	Thr Tyr Asn Tyr Tyr Ser Thr Leu Ser Phe Thr Thr Asp Lys Leu Tyr				
160	50 55 60				
163	Ala Glu Phe Gly Arg Glu Ala Ser Asn Asn Phe Thr Glu Met Ser Gln				
164	65 70 75 80				
167	Arg Leu Glu Ser Met Val Lys Asn Ala Phe Tyr Lys Ser Pro Leu Arg				
168	85 90 95				
171	Glu Glu Phe Val Lys Ser Gln Val Ile Lys Phe Ser Gln Gln Lys His				
172	100 105 110				
175	Gly Val Leu Ala His Met Leu Leu Ile Cys Arg Phe His Ser Thr Glu				
176	115 120 125				
179	Asp Pro Glu Thr Val Asp Lys Ile Val Gln Leu Val Leu His Glu Lys				
180	130 135 140				
183	Leu Gln Asp Ala Val Gly Pro Pro Lys Val Asp Pro His Ser Val Lys				
184	145 150 155 160				
187	Ile Lys Lys Ile Asn Lys Thr Glu Thr Asp Ser Tyr Leu Asn His Cys				
188	165 170 175				
191	Cys Gly Thr Arg Arg Ser Lys Thr Leu Gly Gln Ser Leu Arg Ile Val				
192	180 185 190				
195	Gly Gly Thr Glu Val Glu Glu Gly Glu Trp Pro Trp Gln Ala Ser Leu				
196	195 200 205				
199	Gln Trp Asp Gly Ser His Ala Cys Gly Ala Thr Leu Ile Asn Ala Thr				
200	210 215 220				
203	Trp Leu Val Ser Ala Ala His Cys Phe Thr Thr Tyr Lys Asn Pro Ala				
204	225 230 235 240				
207	Arg Trp Thr Ala Ser Phe Gly Val Thr Ile Lys Pro Ser Lys Met Lys				
208	245 250 255				
211	Arg Gly Leu Arg Arg Ile Ile Val His Glu Lys Tyr Lys His Pro Ser				
212	260 265 270				
215	His Asp Tyr Asp Ile Ser Leu Ala Glu Leu Ser Ser Pro Val Pro Tyr				
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219	Thr Asn Ala Val His Arg Val Cys Leu Pro Asp Ala Ser Tyr Glu Phe				

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227	Asp Gly Tyr Ser Gln Asn His Leu Arg Gln Ala Gln Val Thr Leu Ile			
228	325	330	335	
231	Asp Ala Thr Thr Cys Asn Glu Pro Gln Ala Tyr Asn Asp Ala Ile Thr			
232	340	345	350	
235	Pro Arg Ile Leu Cys Ala Gly Ser Leu Glu Gly Lys Thr Asp Ala Cys			
236	355	360	365	
239	Gln Gly Asp Ser Gly Gly Pro Leu Val Ser Ser Asp Ala Arg Asp Ile			
240	370	375	380	
243	Trp Tyr Leu Ala Gly Ile Val Ser Trp Gly Asp Glu Cys Ala Lys Pro			
244	385	390	395	400
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256	<211> LENGTH: 1269			
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258	<213> ORGANISM: DESC1			
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262	<222> LOCATION: (1)..(1269)			
263	<223> OTHER INFORMATION:			
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269	1 5 10 15			
271	ccc tgg gtt atc ggc ctc gtc atg ttc ata tcc ctg att gtc ctg gca		96	
272	Pro Trp Val Ile Gly Leu Val Met Phe Ile Ser Leu Ile Val Leu Ala			
273	20 25 30			
275	gtg tgc att gga gtc act gtt cat tat gtg aga tat aat caa aag aag		144	
276	Val Cys Ile Gly Val Thr Val His Tyr Val Arg Tyr Asn Gln Lys Lys			
277	35 40 45			
279	acc tac aat tac tat agc aca ttg tca ttt aca act gac aaa cta tat		192	
280	Thr Tyr Asn Tyr Tyr Ser Thr Leu Ser Phe Thr Thr Asp Lys Leu Tyr			
281	50 55 60			
283	gct gag ttt ggc aga gag gct tct aac aat ttt aca gaa atg agc cag		240	
284	Ala Glu Phe Gly Arg Glu Ala Ser Asn Asn Phe Thr Glu Met Ser Gln			
285	65 70 75 80			
287	aga ctt gaa tca atg gtg aaa aat gca ttt tat aaa tct cca tta agg		288	
288	Arg Leu Glu Ser Met Val Lys Asn Ala Phe Tyr Lys Ser Pro Leu Arg			
289	85 90 95			
291	gaa gaa ttt gtc aag tct cag gtt atc aag ttc agt caa cag aag cat		336	
292	Glu Glu Phe Val Lys Ser Gln Val Ile Lys Phe Ser Gln Gln Lys His			
293	100 105 110			
295	gga gtg ttg gct cat atg ctg ttg att tgt aga ttt cac tct act gag		384	
296	Gly Val Leu Ala His Met Leu Leu Ile Cys Arg Phe His Ser Thr Glu			

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308	Ile	Lys	Lys	Ile	Asn	Lys	Thr	Glu	Thr	Asp	Ser	Tyr	Leu	Asn	His	Cys	
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312	Cys	Gly	Thr	Arg	Arg	Ser	Lys	Thr	Leu	Gly	Gln	Ser	Leu	Arg	Ile	Val	
313							180			185			190				
315	ggt	ggg	aca	gaa	gta	gaa	gag	ggt	gaa	tgg	ccc	tgg	cag	gct	agc	ctg	624
316	Gly	Gly	Thr	Glu	Val	Glu	Gly	Glu	Gly	Trp	Pro	Trp	Gln	Ala	Ser	Leu	
317						195			200			205					
319	cag	tgg	gat	ggg	agt	cat	cgc	tgt	gga	gca	acc	tta	att	aat	gcc	aca	672
320	Gln	Trp	Asp	Gly	Ser	His	Arg	Cys	Gly	Ala	Thr	Leu	Ile	Asn	Ala	Thr	
321						210			215			220					
323	tgg	ctt	gtg	agt	gct	gct	cac	tgt	ttt	aca	aca	tat	aag	aac	cct	gcc	720
324	Trp	Leu	Val	Ser	Ala	Ala	His	Cys	Phe	Thr	Thr	Tyr	Lys	Asn	Pro	Ala	
325	225					230				235			240				
327	aga	tgg	act	gct	tcc	ttt	gga	gta	aca	ata	aaa	cct	tcg	aaa	atg	aaa	768
328	Arg	Trp	Thr	Ala	Ser	Phe	Gly	Val	Thr	Ile	Lys	Pro	Ser	Lys	Met	Lys	
329						245			250			255					
331	cgg	ggt	ctc	cgg	aga	ata	att	gtc	cat	gaa	aaa	tac	aaa	cac	cca	tca	816
332	Arg	Gly	Leu	Arg	Arg	Ile	Ile	Val	His	Glu	Lys	Tyr	Lys	His	Pro	Ser	
333						260			265			270					
335	cat	gac	tat	gat	att	tct	ctt	gca	gag	ctt	tct	agc	cct	gtt	ccc	tac	864
336	His	Asp	Tyr	Asp	Ile	Ser	Leu	Ala	Glu	Leu	Ser	Ser	Pro	Val	Pro	Tyr	
337						275			280			285					
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343	caa	cca	ggt	gat	gtg	atg	ttt	gtg	aca	gga	ttt	gga	gca	ctg	aaa	aat	960
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352	Asp	Ala	Thr	Thr	Cys	Asn	Glu	Pro	Gln	Ala	Tyr	Asn	Asp	Ala	Ile	Thr	
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355	cct	aga	atg	tta	tgt	gct	ggc	tcc	tta	gaa	gga	aaa	aca	gat	gca	tgc	1104
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357						355			360			365					
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361						370			375			380					

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